LR-4610
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RESEARCH ARTICLE Legume Research- An International Journal, Volume Issue : ()

Assessment of Genetic Variability and Relationship between Different Quantitative Traits in Field Pea (*Pisum sativum* var. *arvense*) Germplasm

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10.18805/LR-4610

ABSTRACT

Background: Assessment of genetic variability and inter-relationship between the characters can be used in the breeding programme to evolve new varieties with wide genetic diversity to maximize the yield potential in crop improvement programmes. Eighty-four field pea genotypes were evaluated in an augmented block design for thirteen quantitative traits to study variance components, heritability, genetic advance and inter-relationship between the yield and yield contributing traits.

Methods: The extent of phenotypic and genotypic variation that exist in a character was calculated by the formula suggested by Burton and de Vane (1953). Heritability in broad sense and genetic advance as per cent of mean for each character was computed using the formula suggested by Hanson *et al.* (1956) and Johnson *et al.* (1955), respectively. Correlation coefficient was calculated by method suggested by Searle (1961) and path coefficient analysis done as per method of Wright (1921) and elaborated by Dewey and Lu (1959).

Result: Significant differences observed among the genotypes tested for the yield characters indicated the presence of variability. High heritability coupled with high genetic advance as percent of mean was observed for the traits *viz.,* plant height, effective pods plant^{-1}, harvest index and seed yield plant^{-1} were governed by additive gene effects which will aid in effective selection. Correlation coefficient analysis revealed that seed yield plant^{-1} had highly significant and positive correlation with biological yield plant^{-1}, effective pods plant^{-1}, harvest index, seeds pods^{-1} and effective nodes plant^{-1}, indicating that these traits are strongly associated with seed yield in field pea. Path coefficient analysis identified biological yield plant^{-1} followed by harvest index, seed pod^{-1}, effective nodes plant^{-1}, 100-seed weight and day to 50% flowering as highly desirable components with great direct effects on seed yield.

Key words: Correlation, Field pea, GCV, Path coefficient, PCV.

INTRODUCTION

Field pea (*Pisum sativum* var. *arvense*) is an autogamous winter season legume which belongs to the family *Fabaceae* (*Leguminosae*). Nutritionally, it is also a rich source of protein (21-25%) with higher concentration of lysine and tryptophan amino acids (Gregory *et al*. 2016) and with low level of cysteine and methionine amino acids (Ceyhan and Avci, 2005). Additionally, pea also have starch (20-25%), sugar (4-10%), fat (0.6-1.5 %) and minerals (2-4%) (Makasheva, 1983). The area and production of field pea in India during 2017-18 was around 8.2 lakh hectares and 9.87 lakh tonnes with an annual productivity of 1204 kg/ha (Anonymous, 2019). In India, Uttar Pradesh and Madhya Pradesh are the leading states producing field pea and the country has the largest cultivated area under pulses in the world, but the average productivity is very low and the production is insufficient to meet the per capita requirement. In total output of pulses, a quantum hike is required to increase the availability per capita and to meet the challenges of increasing population. Therefore, high yielding field pea varieties and good quality seed are essential to sustain its production.

In any crop improvement programme, there is need to focus on creation of genetic variability and selection for important characters for the improvement of yield and their component traits. However, information of available genetic diversity among field pea germplasm, the nature of component traits on which selection will be effective and the effect of environmental factors on each trait must be understood in order to carry out effective selection (Jaleta *et al*., 2011). The estimates of genetic variability coupled with heritability gives a clear idea of genetic advance to be expected from selection (Burton, 1952), while heritability along with genetic advance aids to draw useful conclusion for effective selection based on phenotypic performance.

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How to cite this article: Pratap, V., Sharma, V., Kamaluddin and Shukla, G. (2021). Assessment of Genetic Variability and Relationship between Different Quantitative Traits in Field Pea (*Pisum sativum* var. *arvense*) Germplasm. Legume Research. DOI: 10.18805/LR-4610.

Submitted: 15-03-2021 **Accepted:** 12-05-2021 **Online:** 27-05-2021

The estimates of high genetic advance along with high heritability offer the most effective condition for selection (Larik *et al*., 2000). In the plant system, most of the traits are inter-related to each other and sometimes change in one trait is likely to affect the other. Therefore, the expression of yield in plants relies on the behaviour and interaction of a range of important traits (Elias, 1992). The understanding of the relationship of characters is of primary importance in the planning of an effective breeding programme. Correlation analysis give information on the association of any two characters. Since, simple correlation analysis is not capable of offering detailed and actual information of the relationship between dependent variables and predictor variables, path analysis has been studied in most of causation relationships. Therefore, study of correlation along with path coefficient analysis is more useful to study the yield contributing traits (Mahajan *et al*., 2011).

MATERIALS AND METHODS

Eighty diverse field pea genotypes along with four checks (IPF 4-9, Adarsh, Ambika and IPFD 10-12) were obtained from ICAR-IIPR, Kanpur; CSAUAT, Kanpur and CCSHAU, Hisar. The experimental material was evaluated in an augmented block design during *rabi*, 2019-20 at Research Farm of Banda University of Agriculture and Technology, Banda. The whole experimental site was divided into eight blocks and each block had fourteen plots. In each block, ten plots accommodate test genotypes (not replicated), whereas remaining four plots were allocated to checks. Each plot consists of single row of genotypes with 5m length and spacing of 30 x10 cm. The observations were recorded for 13 quantitative traits *viz*., days to 50 % flowering (DF), days to maturity (DM), plant height (PH), number of branches plant^{-1} (NB), number of nodes plant^{-1} (NN), number of effective nodes plant^{-1} (NEN), number of effective pods plant^{-1} (NEP), number of seeds plant^{-1} (SP), pod length (PL), 100-seed weight (SW), seed yield plant^{-1} (SY), biological yield plant^{-1} (BY) and harvest index (HI). The extent of phenotypic and genotypic variation that exist in a character was calculated by the formula suggested by Burton and de Vane (1953). Heritability (h^2) in broad sense and Genetic advance as per cent of mean (GAM) for each character was computed using the formula suggested by Hanson *et al*. (1956) and Johnson *et al*. (1955), respectively. Correlation coefficient was calculated by method suggested by Searle (1961) and path coefficient analysis done as per method of Wright (1921) and elaborated by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance showed existence of sufficient variability within the evaluated germplasm lines for all the thirteen characters under analysis. The estimates of PCV, GCV, heritability and genetic advance for various characters are given in Table 1.

The estimates of PCV was greater than GCV for all the 13 characters which indicates considerable impact of environment on the expression of these traits. The maximum amount of PCV and GCV were recorded for traits like plant height, branches plant^{-1}, effective nodes plant^{-1}, effective pods plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1}. High GCV values suggested that the possibility of improving these traits through selection means these characters may be utilized as selection parameters. In addition to above traits, seed pod^{-1} and harvest index showed high PCV as well as moderate GCV. Day to maturity and 50 % flowering showed low values of PCV and GCV. Whereas all the remaining characters showed moderate PCV and GCV. In the previous studies, higher estimates of PCV and GCV was reported Gour *et al*. (2018) for branches plant^{-1}, plant height, effective node plant^{-1}, effective pod plant^{-1}, biological yield plant^{-1} and seed yield plant^{-1}.

The greater difference between value of PCV and GCV was recorded for branches plant^{-1}, seed pod^{-1} and biological yield. This also suggested the influence of these traits by environment. However, the least difference between PCV and GCV was observed for days to maturity and 50% flowering, which indicated the least impact of environment on the expression of these traits. These findings are in accordance with Lal *et al*. (2018).

The heritability estimate was high for plant height, effective pod plant^{-1}, harvest index and seed yield plant^{-1}, indicating that selection for these traits could be very easy. This is because there would be a close correspondence between the genotype and phenotype due to the comparatively limited contribution of the environment to the phenotype. Similar results of heritability were concluded by Meena *et al*. (2017) for plant height, pods plant^{-1} and seed yield plant^{-1}.

The high genetic advance as percent of mean found for effective pods plant^{-1}, seed yield plant^{-1}, biological yield plant^{-1}, plant height, effective nodes plant^{-1}, nodes plant^{-1}, 100 seed weight and seeds pod^{-1}, moderate GAM were recorded for days to 50 % flowering and pod length. Days to maturity showed low genetic gain. Estimation of heritability along with genetic advance is helpful in predicting gain under selection (Johnson *et al*. 1955). The present study indicates high heritability coupled with high genetic advance as percent of mean for plant height, effective pods plant^{-1}, harvest index and seed yield plant^{-1} which implies that these traits were governed by additive gene effects and selection may be easy and effective. The similar results were reported by Meena *et al.* (2017) and Ton *et al*. (2018).

Correlation coefficients analysis

Correlation studies offers an opportunity to assess the interaction of different traits with seed yield. It will be very helpful to recognize suitable yield components and draw information about their interrelationship with yield and also each other for the development of variety with high yield potential. The values of correlation coefficients among thirteen traits of field pea and its correlation matrix showing association of different characters with each other are

Table 1: Estimates of variability parameters for different characters of field pea germplasm

Characters	PCV (%)	GCV (%)	(h^2)	GA	GAM
Days to 50% flowering	7.15	6.09	72.63	7.80	10.70
Days to maturity	2.05	1.53	55.97	2.68	2.36
Plant height (cm)	27.96	26.77	91.68	74.07	52.81
Number of branches plant^{-1}	40.62	27.99	47.48	1.30	39.73
Number of nodes plant^{-1}	17.22	14.95	75.37	4.08	26.74
Number of effective nodes plant^{-1}	31.38	27.15	74.86	2.83	48.40
Number of effective pods plant^{-1}	43.93	41.46	89.04	18.26	80.59
Number of seeds pod^{-1}	22.29	14.97	45.11	0.94	20.71
Pod length (cm)	16.05	11.96	55.5	1.08	18.35
100-seed weight (g)	17.32	14.01	65.42	3.48	23.34
Biological yield plant^{-1} (g)	39.10	34.01	75.63	24.05	60.92
Harvest index (%)	21.37	19.27	81.34	11.40	35.80
Seed yield plant^{-1} (g)	46.30	41.55	80.53	9.78	76.80

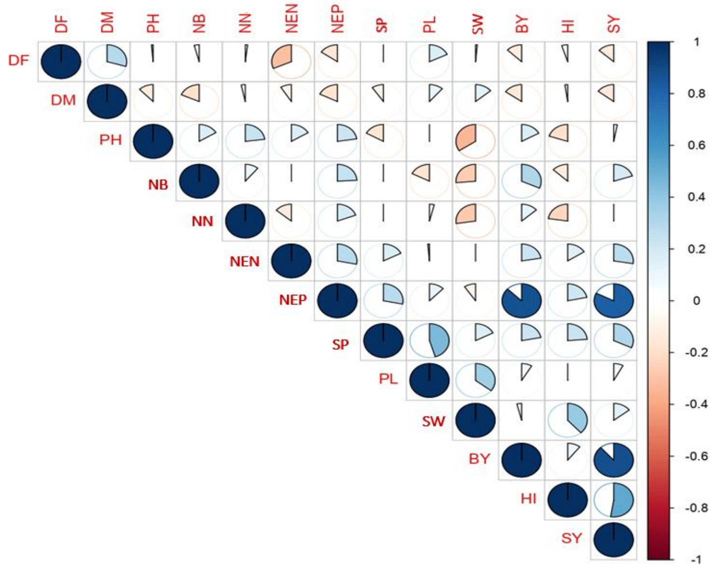

Fig 1: Diagrammatic representation of correlation between different quantitative traits in field pea.

presented in Table 2. The area of the circle is relatively proportional to the correlation between the characters (Fig 1).

In this investigation, correlation coefficients revealed that seed yield plant^{-1} showed strong and positive association with biological yield plant^{-1}, effective pods plant^{-1}, harvest index, seeds pods^{-1} and effective nodes plant^{-1}. Thus, biological yield plant^{-1}, effective pods plant^{-1}, harvest index, seeds pod^{-1} and effective nodes plant^{-1} emerged as closely correlated yield attributes and indicated scope for improving seed yield through simultaneous selection. Whereas, seed yield plant^{-1} was non-significant and negatively associated with days to 50% flowering and maturity. Similar findings for seed yield with one or more of the above traits has also reported by Lal *et al.* (2018) and Kumawat *et al*. (2018).

These characters also showed strong positive association with other traits *i.e.* biological yield plant^{-1} showed strong association with effective pods plant^{-1}, branches plant^{-1}, effective nodes plant^{-1} and seed pod^{-1}. Similarly, effective pods plant^{-1} had strong correlation with biological yield plant^{-1}, seed pod^{-1}, effective nodes plant^{-1}, branches plant^{-1}, plant height and harvest index. Harvest index showed highly strong association with seeds pod^{-1} and effective pods plant^{-1}. Seeds pod^{-1} had highly strong correlation with pod length, effective pods plant^{-1}, harvest index and biological yield. Effective nodes plant^{-1} had strong correlation with effective pods plant^{-1} and biological yield plant^{-1}. The correlation coefficient gives a symmetrical estimate of the degree of interaction between two characters, helps to explain the magnitude of the interaction among the yield and its components. From this point of view, knowledge on inter-relationship between seed yield and associated traits is a prerequisite for the creation of an efficient selection strategy aimed at improving seed yield.

Table 2: Estimates of correlation coefficient between different quantitative traits in field pea germplasm.

Characters	DF	DM	PH	NB	NN	NEN	NEP	SP	PL	SW	BY	HI	SY
DF	1.000	0.295**	-0.014	-0.042	0.019	-0.316**	-0.154	0.007	0.179	0.014	-0.129	-0.050	-0.134
DM		1.000	-0.122	-0.184	-0.034	-0.090	-0.178	-0.097	0.113	0.140	-0.152	-0.023	-0.146
PH			1.000	0.163	0.230*	0.164	0.226*	-0.169	0.006	-0.343**	0.170	-0.200	0.029
NB				1.000	0.111	-0.007	0.241*	-0.005	-0.175	-0.264*	0.317**	-0.132	0.200
NN					1.000	-0.140	0.193	-0.007	0.039	-0.274*	0.136	-0.226*	0.002
NEN						1.000	0.282**	0.175	-0.014	0.001	0.224*	0.159	0.276*
NEP							1.000	0.282**	0.123	-0.095	0.872**	0.218*	0.825**
SP								1.000	0.452**	0.175	0.221*	0.237*	0.319**
PL									1.000	0.354**	0.086	0.002	0.079
SW										1.000	-0.039	0.382	0.146
BY											1.000	0.106	0.885**
HI												1.000	0.526**
SY													1.000

*,** Significant at 5% and 1% level of significance, respectively.

Table 3: Estimates of direct effect and indirect effect of different quantitative characters on seed yield in field pea germplasm.

Characters	Direct effect	Indirect effect											
		DF	DM	PH	NB	NN	NEN	NEP	SP	PL	SW	BY	HI	SY
DF	0.0048		-0.0031	0.0003	0.0003	-0.0001	-0.0066	0.0009	0.0002	-0.002	0.0001	-0.1084	-0.0207	-0.1343
DM	-0.0105	0.0014		0.0029	0.0015	0.0002	-0.0019	0.0011	-0.0031	-0.0013	0.001	-0.1280	-0.0095	-0.1463
PH	-0.0235	-0.0001	0.0013		-0.0013	-0.0011	0.0034	-0.0013	-0.0053	-0.0001	-0.0025	0.1430	-0.0833	0.0292
NB	-0.008	-0.0002	0.0019	-0.0038		-0.0005	-0.0001	-0.0014	-0.0001	0.002	-0.0019	0.2667	-0.0548	0.1997
NN	-0.0049	0.0001	0.0004	-0.0054	-0.0009		-0.0029	-0.0011	-0.0002	-0.0004	-0.002	0.1143	-0.0944	0.0024
NEN	0.021	-0.0015	0.001	-0.0038	0.0001	0.0007		-0.0017	0.0055	0.0002	0.000	0.1884	0.0665	0.2763
NEP	-0.0059	-0.0007	0.0019	-0.0053	-0.0019	-0.0009	0.0059		0.0089	-0.0014	-0.0007	0.7340	0.0908	0.8246
SP	0.0316	0.000	0.001	0.004	0.000	0.000	0.0037	-0.0017		-0.0051	0.0013	0.1856	0.0989	0.3195
PL	-0.0112	0.0009	-0.0012	-0.0002	0.0014	-0.0002	-0.0003	-0.0007	0.0143		0.0026	0.0724	0.0008	0.0786
SW	0.0074	0.0001	-0.0015	0.008	0.0021	0.0013	0.000	0.0006	0.0055	-0.004		-0.0329	0.1593	0.146
BY	0.8412	-0.0006	0.0016	-0.004	-0.0025	-0.0007	0.0047	-0.0052	0.007	-0.001	-0.0003		0.0443	0.8847
HI	0.4170	-0.0002	0.0002	0.0047	0.001	0.0011	0.0034	-0.0013	0.0075	0.000	0.0028	0.0894		0.5256

Residual factor = 0.163.

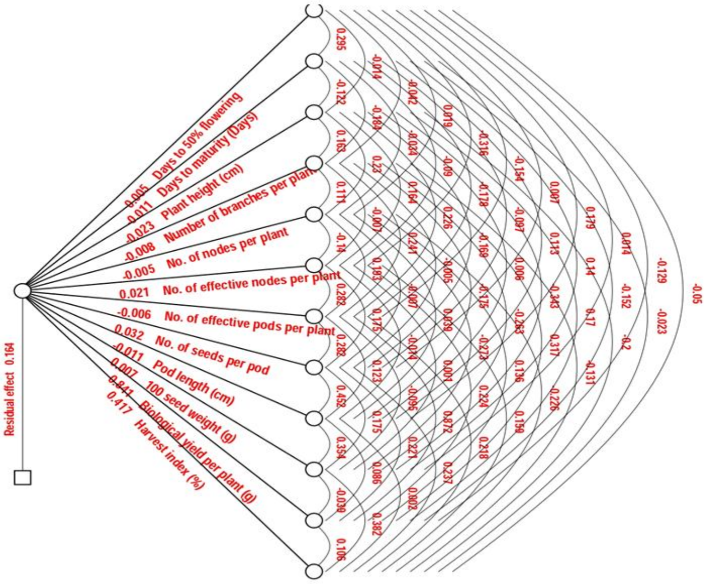

Fig 2: Representation of direct effect and indirect effect of different quantitative characters on seed yield

Path coefficient analysis

Path co-efficient analysis tests the causal influence of one character on the other and allows partitioning of the correlation co-efficient into direct and indirect effects. This gives actual information on the contribution of the characters and thus forms the basis for the selection of yield contributing traits to improve the yield. The estimates of direct and indirect effects of twelve characters on seed yield plant^{-1} determined under path coefficient analysis using correlation coefficient are shown in Table 3 and depicted graphically in Fig 2.

A perusal of Table 2 demonstrated that highest positive direct effect on seed yield plant^{-1} were exerted by biological yield plant^{-1}, followed by harvest index, seed pod^{-1}, effective nodes plant^{-1}, 100-seed weight and 50 % day to flowering. This clearly illustrates the fact that the change in each of the above characters will directly contribute to the yield of the crop. Similarly finding for above traits have been reported by Tofiq *et al*. (2015), Lal *et al*. (2018) and Ton *et al*. (2018). However, other characters contributing substantially positive direct effect on seed yield were seeds pod^{-1}, effective nodes plant^{-1}, 100-seed weight and days to 50% flowering.

Highly positive indirect effects on seed yield were exhibited by effective pods plant^{-1}, branch plant^{-1}, effective nodes plant^{-1}, seed pod^{-1}, plant height, nodes plant^{-1}, harvest index and pod length via biological yield plant^{-1}. This suggests that these characters supplemented greatly to the seed yield by the biological yield plant^{-1}. Similarly, 100-seed weight, seeds pod^{-1}, effective pods plant^{-1}, effective nodes plant^{-1}, biological yield plant^{-1} and pod length exerts positive indirect effect on seed yield via harvest index. In contrast, days to maturity and days to 50% flowering via biological yield plant^{-1}; nodes plant^{-1} and plant height, branches plant^{-1}, days to 50% flowering via harvest index showed highly negative indirect effect on seed yield plant^{-1}. The residual estimates of indirect effects were low in this study. These results have been in line with Tofiq *et al*. (2015) and Ton *et al*. (2018).

Hence from path analysis, it could be concluded that harvest index, seeds pod^{-1} and effective nodes plant^{-1} contributed to seed yield directly as well as indirectly. These characters also had moderate to high estimate of variability parameters which were correlated strongly with each other. Therefore, due emphasis should be placed on these characters while formulating selection strategy in field pea for developing high yielding varieties.

In formulating a selection strategy for the development of high yielding field pea varieties, the characters referred to above as significant direct and indirect contributors to the yield are useful for consideration. The collection and assessment of new germplasm material is important for the exploration of new valuable genotypes to be used in the breeding programmes to integrate favourable genes into the desirable genetic context for the production of new improved varieties.

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